

*BLAST SEARCH**SEG ID # 16*Distance tree of results NEW

Sequences producing significant alignments:		Score (Bits)	E Value
gb ABD61942.1 	ORF1 [Torque teno virus]	29.1	34
emb CAJ88088.1 	putative secreted esterase [Streptomyces ambo...	28.6	46
ref XP_635992.1 	hypothetical protein DDBDRAFT_0188654 [Dicty...	28.6	46
ref NP_242669.1 	hypothetical protein BH1803 [Bacillus halodu...	28.2	61
ref ZP_01170405.1 	hypothetical protein B14911_27995 [Bacillu...	28.2	61
ref YP_001391336.1 	SCP-like extracellular protein [Clostridi...	27.8	82
ref ZP_01925098.1 	hypothetical protein VvadDRAFT_1379 [Victi...	27.8	82
ref ZP_01860086.1 	hypothetical protein BSG1_13771 [Bacillus ...	27.8	82
ref ZP_01858224.1 	hypothetical protein BSG1_01850 [Bacillus ...	27.8	82
ref ZP_01860745.1 	hypothetical protein BSG1_19909 [Bacillus ...	27.8	82
ref YP_001254514.1 	exported protein [Clostridium botulinum A...	27.8	82
ref ZP_01723449.1 	hypothetical protein BB14905_01215 [Bacill...	27.8	82
ref NP_782890.1 	transporter [Clostridium tetani E88] >gb AAO...	27.8	82
ref NP_109933.1 	peptide deformylase [Mycoplasma pneumoniae M...	27.8	82
ref NP_691788.1 	hypothetical protein OB0867 [Oceanobacillus ...	27.8	82
ref ZP_01170447.1 	hypothetical protein B14911_28205 [Bacillu...	27.8	82
ref ZP_01170733.1 	YkwD [Bacillus sp. NRRL B-14911] >gb EAR66...	27.8	82
ref YP_001179948.1 	Allergen V5/Tpx-1 family protein [Caldice...	27.8	82
ref YP_001036731.1 	Allergen V5/Tpx-1 related [Clostridium th...	27.8	82
ref NP_899531.1 	conserved hypothetical protein [Vibrio phage...	27.4	110
ref ZP_00630756.1 	conserved hypothetical protein [Paracoccus...	27.4	110
ref XP_391385.1 	hypothetical protein FG11209.1 [Gibberella zeae	27.4	110
ref YP_432181.1 	predicted membrane protein [Hahella chejuens...	26.9	148
ref XP_567377.1 	S-adenosylmethionine-dependent methyltransfe...	26.9	148
ref YP_269817.1 	hypothetical protein CPS_3120 [Colwellia psy...	26.5	198
ref NP_769389.1 	probable C4-dicarboxylate-binding protein [B...	26.5	198
ref XP_001332573.1 	PREDICTED: similar to LOC733311 protein [Dan	25.7	357
ref XP_001332460.1 	PREDICTED: similar to LOC733311 protein [Dan	25.7	357
ref XP_001332004.1 	PREDICTED: hypothetical protein [Danio rerio	25.7	357
ref XP_001307448.1 	hypothetical protein TVAG_219240 [Trichom...	25.7	357
gb ABB22239.1 	thymidine kinase-like protein [Ovine herpesvirus	25.7	357
gb ABK63686.1 	phenylpropionate dioxygenase [uncultured bacteriu	25.7	357
ref ZP_01424440.1 	hypothetical protein HaurDRAFT_3556 [Herpe...	25.7	357
ref ZP_01224243.1 	probable lipoprotein signal peptide [marin...	25.7	357
ref XP_457843.1 	hypothetical protein DEHA0C04268g [Debaryomy...	25.7	357
ref YP_438145.1 	ORF21 [Ovine herpesvirus 2] >gb AAX58057.1 ...	25.7	357
dbj BAF66141.1 	NADH dehydrogenase subunit 4 [Eumetopias jubatus	25.2	479
emb CAI22213.1 	phosphoglycerate dehydrogenase [Homo sapiens]...	25.2	479
ref XP_001504201.1 	PREDICTED: similar to v-ros UR2 sarcoma v...	25.2	479
ref XP_001498877.1 	PREDICTED: similar to protein regulating ...	25.2	479
ref XP_001518175.1 	PREDICTED: similar to proto-oncogene c-ro...	25.2	479
gb EDL92942.1 	v-ros UR2 sarcoma virus oncogene homolog 1 (av...	25.2	479
gb EDL05073.1 	Ros1 proto-oncogene, isoform CRA_a [Mus musculus]	25.2	479
gb EDL05074.1 	Ros1 proto-oncogene, isoform CRA_b [Mus musculus]	25.2	479
dbj BAF62930.1 	NADH dehydrogenase subunit 4 [Eumetopias juba...	25.2	479

ref XP_001593909.1 	hypothetical protein SS1G_05337 [Scleroti...	24.4	863
ref XP_001554485.1 	hypothetical protein BC1G_07073 [Botryoti...	24.4	863
ref ZP_01891743.1 	putative lipopolysaccharide biosynthesis p...	24.4	863
ref YP_861439.1 	cbb3-type cytochrome c oxidase subunit I [Gr...	24.4	863
gb EAT85328.1 	hypothetical protein SNOG_07862 [Phaeosphaeria no	24.4	863
gb AAW26476.1 	SJCHGC01111 protein [Schistosoma japonicum]	24.4	863
ref YP_084687.1 	possible glycosyl hydrolase [Bacillus cereus...	24.4	863

Alignments

>**gb|ABD61942.1|** ORF1 [Torque teno virus]
Length=732

Score = 29.1 bits (61), Expect = 34
Identities = 7/9 (77%), Positives = 9/9 (100%), Gaps = 0/9 (0%)

Query 1 KPAQYWTQM 9
KPA+YWTQ+
Sbjct 284 KPAEYWTQL 292

>**emb|CAJ88088.1|** putative secreted esterase [Streptomyces ambofaciens ATCC 23877]
Length=499

Score = 28.6 bits (60), Expect = 46
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 PAQYWTQ 8
PAQYWTQ
Sbjct 339 PAQYWTQ 345

>**ref|XP_635992.1|** **G** hypothetical protein DDBDRAFT_0188654 [Dictyostelium discoid
AX4]

gb|EAL62481.1| **G** hypothetical protein DDBDRAFT_0188654 [Dictyostelium discoideu
AX4]
Length=871

Score = 28.6 bits (60), Expect = 46
Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 4 QYWTQMFY 11
QYW +MFY
Sbjct 247 QYWNEMFY 254

>**ref|NP_242669.1|** **G** hypothetical protein BH1803 [Bacillus halodurans C-125]

dbj|BAB05522.1| **G** BH1803 [Bacillus halodurans C-125]
Length=207

Score = 28.2 bits (59), Expect = 61
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 4 QYWTQMF 10
YWTQMF
Sbjct 198 HYWTQMF 204

>**ref|ZP_01170405.1|** hypothetical protein B14911_27995 [Bacillus sp. NRRL B-14911]
gb|EAR66924.1| hypothetical protein B14911_27995 [Bacillus sp. NRRL B-14911]
Length=207

Score = 28.2 bits (59), Expect = 61
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

*BLAST SEARCH**SEQ ID #19*Distance tree of results NEW

Sequences producing significant alignments:			Score (Bits)	E Value
ref NP_691788.1	hypothetical protein OB0867 [Oceanobacillus ...		29.9	19
ref NP_612690.1	tegument protein UL47 [Chimpanzee cytomegalo...		29.5	25
ref YP_001179948.1	Allergen V5/Tpx-1 family protein [Caldice...		28.6	46
ref XP_635992.1	hypothetical protein DDBDRAFT_0188654 [Dicty...		28.6	46
ref YP_211922.1	hypothetical protein BF2300 [Bacteroides fra...		28.2	61
ref NP_242669.1	hypothetical protein BH1803 [Bacillus halodu...		28.2	61
ref ZP_01170405.1	hypothetical protein B14911_27995 [Bacillu...		28.2	61
ref ZP_01170733.1	Ykwd [Bacillus sp. NRRL B-14911] >gb EAR66...		28.2	61
ref YP_001391336.1	SCP-like extracellular protein [Clostridi...		27.8	82
ref ZP_01860086.1	hypothetical protein BSG1_13771 [Bacillus ...		27.8	82
ref ZP_01858224.1	hypothetical protein BSG1_01850 [Bacillus ...		27.8	82
ref ZP_01860745.1	hypothetical protein BSG1_19909 [Bacillus ...		27.8	82
ref YP_001254514.1	exported protein [Clostridium botulinum A...		27.8	82
ref ZP_01723449.1	hypothetical protein BB14905_01215 [Bacill...		27.8	82
ref NP_782890.1	transporter [Clostridium tetani E88] >gb AAO...		27.8	82
ref NP_109933.1	peptide deformylase [Mycoplasma pneumoniae M...		27.8	82
ref ZP_01170447.1	hypothetical protein B14911_28205 [Bacillu...		27.8	82
ref YP_001036731.1	Allergen V5/Tpx-1 related [Clostridium th...		27.8	82
ref YP_861439.1	cbb3-type cytochrome c oxidase subunit I [Gr...		27.4	110
ref XP_391385.1	hypothetical protein FG11209.1 [Gibberella zeae		27.4	110
ref YP_432181.1	predicted membrane protein [Hahella chejuens...		26.9	148
ref XP_001638630.1	predicted protein [Nematostella vectensis...		26.5	198
ref XP_001539048.1	predicted protein [Ajellomyces capsulatus...		26.5	198
ref YP_269817.1	hypothetical protein CPS_3120 [Colwellia psy...		26.5	198
ref NP_769389.1	probable C4-dicarboxylate-binding protein [B...		26.5	198
gb EAA28794.2	hypothetical protein NCU09115 [Neurospora crassa		26.1	266
gb ABP87526.1	NADH dehydrogenase subunit 2 [Anolis cristatel...		26.1	266
ref ZP_02014054.1	hypothetical protein ObacDRAFT_2737 [Opitu...		26.1	266
ref ZP_01922988.1	hypothetical protein VvadDRAFT_2084 [Victi...		26.1	266
gb ABB22239.1	thymidine kinase-like protein [Ovine herpesvirus		26.1	266
ref NP_825172.1	hypothetical protein SAV3995 [Streptomyces a...		26.1	266
ref YP_438145.1	ORF21 [Ovine herpesvirus 2] >gb AAX58057.1 ...		26.1	266
ref XP_958030.1	hypothetical protein [Neurospora crassa OR74A]		26.1	266
gb EAL41048.3	AGAP010349-PA [Anopheles gambiae str. PEST]		25.7	357
gb EDO59982.1	hypothetical protein CLOLEP_02799 [Clostridium le		25.7	357
ref XP_001600764.1	PREDICTED: similar to conserved hypotheti...		25.7	357
emb CAM98568.1	NADH4 protein [Ailuropoda melanoleuca]		25.7	357
gb EDN61082.1	multidrug transporter [Saccharomyces cerevisiae Y		25.7	357
ref YP_001249293.1	NADH dehydrogenase subunit 4 [Ailuropoda ...		25.7	357
ref ZP_01815912.1	hypothetical protein VSWAT3_15599 [Vibrion...		25.7	357
ref XP_001444812.1	hypothetical protein [Paramecium tetraure...		25.7	357
ref ZP_01640763.1	peptidase S9, prolyl oligopeptidase active...		25.7	357
ref YP_829511.1	glycosyl transferase, family 2 [Arthrobacter...		25.7	357
ref XP_559110.2	ENSANGP00000027759 [Anopheles gambiae str. PEST		25.7	357
ref YP_778730.1	NADH dehydrogenase subunit 4 [Phocarctos hoo...		25.7	357
gb EAT85328.1	hypothetical protein SNOG_07862 [Phaeosphaeria no		25.7	357

>ref|NP_691788.1| **G** hypothetical protein OB0867 [Oceanobacillus iheyensis HTE831
 dbj|BAC12823.1| **G** hypothetical conserved protein [Oceanobacillus iheyensis HTE8
 Length=278

Score = 29.9 bits (63), Expect = 19
 Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 3/12 (25%)

Query 2 HVQ---YWTQMF 10
 HV+ YWTQMF
 Sbjct 264 HVENGNYWTQMF 275

>ref|NP_612690.1| **G** tegument protein UL47 [Chimpanzee cytomegalovirus]
 gb|AAM00696.1|AF480884_48 **G** tegument protein UL47 [chimpanzee cytomegalovirus]
 Length=982

Score = 29.5 bits (62), Expect = 25
 Identities = 9/13 (69%), Positives = 9/13 (69%), Gaps = 2/13 (15%)

Query 2 HVQYW--TQMFYT 12
 HV YW T MFYT
 Sbjct 210 HVTYWACTLMFYT 222

>ref|YP_001179948.1| **G** Allergen V5/Tpx-1 family protein [Caldicellulosiruptor sa
 DSM 8903]

gb|ABP66757.1| **G** Allergen V5/Tpx-1 family protein [Caldicellulosiruptor sacchar
 DSM 8903]
 Length=203

Score = 28.6 bits (60), Expect = 46
 Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 3 VQYWTQMF 10
 V YWTQMF
 Sbjct 192 VLYWTQMF 199

>ref|XP_635992.1| **G** hypothetical protein DDBDRAFT_0188654 [Dictyostelium discoid
 AX4]

gb|EAL62481.1| **G** hypothetical protein DDBDRAFT_0188654 [Dictyostelium discoideu
 AX4]
 Length=871

Score = 28.6 bits (60), Expect = 46
 Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 4 QYWTQMFY 11
 QYW +MFY
 Sbjct 247 QYWNEMFY 254

>ref|YP_211922.1| **G** hypothetical protein BF2300 [Bacteroides fragilis NCTC 9343]

emb|CAH07994.1| **G** putative membrane protein [Bacteroides fragilis NCTC 9343]
 Length=166

Score = 28.2 bits (59), Expect = 61
 Identities = 8/15 (53%), Positives = 8/15 (53%), Gaps = 6/15 (40%)

Query 4 QYWTQM-----FYT 12
 QYW QM FYT
 Sbjct 117 QYWIQMTDKGEKFYT 131